

Quantitative Comparison of Artificial Honey Bee Colony Clustering and Enhanced SOM based K-means Clustering Algorithms for Extraction of ROI from Breast DCE-MR Images

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Abstract—This paper introduces a comparison of two popular clustering algorithms for breast DCE-MRI segmentation purpose. Magnetic resonance imaging (MRI) is an advanced medical imaging technique providing rich information about the human soft tissue anatomy. The goal of breast magnetic resonance image segmentation is to accurately identify the principal mass or lesion structures in these image volumes. There are many methods that exist to segment the breast DCE-MR images. One of these, K-means clustering procedure provides effective solutions in many science and engineering fields. They are especially popular in the pattern classification and signal processing areas and can segment the breast DCE-MRI with high precision. The artificial bee colony (ABC) algorithm is a new, very simple and robust population based optimization algorithm that is inspired by the intelligent behavior of honey bee swarms. This paper compares the performance of two image segmentation techniques in the subject of breast DCE-MR image. In the experiments, the real dynamic contrast enhanced magnetic resonance images (DCE- MRI) are used. Results show that artificial bee colony algorithm performs better in terms of segmentation accuracy, robustness and speed of computation.

Index Terms— Breast DCE-MRI; Artificial Bee Colony clustering, Enhanced SOM based K-means clustering.

I. INTRODUCTION

Breast cancer is one of the major causes of death among women. Early diagnosis through regular screening and timely treatment has been revealed to prevent breast cancer. The framework is to develop tools acting as a support to the diagnosis process for those affections that require medical imaging. Such tools present to the clinician both a qualitative and a quantitative description of the disease and allow him to formulate more detailed diagnoses. Besides, it is possible to better follow the evolution of the particular syndrome investigated because comparisons can be easily carried out between successive tests for the same patient. The application of medical image processing techniques has rapidly increased in recent years. Medical images almost are stored and represented digitally [1]. Magnetic resonance imaging is an important diagnostic imaging technique to obtain high quality breast images in both clinical and research areas because it is

virtually non-invasive and it possesses a high spatial resolution and an excellent contrast of soft tissues [2- 4]. MR images are widely used not only for detecting tissue deformities such as cancers and injuries, but also for studying breast pathology [5]. In order to offer useful and accurate clinical information, the segmentation and recognition algorithms of MR images are becoming an important subject of the study on medical image processing. In segmenting MRI data, we have mainly three considerable difficulties: noise, partial volume effects (where more than one tissue is inside a pixel volume) and intensity inhomogeneity [3]. Noise in MR images can induce segmentation regions to become disconnected. Therefore, it is important to take advantage of useful data while at the same time overcoming potential difficulties [6, 7].

The aim of this paper is to compare the performance of artificial bee colony clustering algorithm with the Enhanced SOM based K – means clustering algorithm to segment breast DCE- MR images. And provide a quantitative comparison of the performance of these image segmentation techniques in subject of breast DCE-MR images. The remainder of this paper is organized as follows. Section 2 illustrates the description of Enhanced SOM based K – means clustering algorithm for breast DCE- MRI and the detail explanation of artificial bee colony algorithm based clustering breast DCE- MRI. Result and discussion are reported in Section 3. The conclusion is summed up in Section 4.

II. MATERIALS AND METHODS

Medical image segmentation has a very important rule in many computer assisted diagnostic tools. These tools could save clinicians time by simplifying the time consuming process. Main part of these tools is to design an efficient segmentation algorithm. Medical images mostly contain unknown noise, in-homogeneity and images is a challenging and complex task. Medical image segmentation has been an active research area for a long time. There are many segmentation algorithms [2, 6, 8 -14] for breast DCE-MR images, but the research for a generic algorithm for totally successful segmentation of breast MR images is still in

progress. Computer based segmentation has reminded largely an experimental work.

A. The Enhanced Self-Organizing Features Map based K-means Clustering Algorithm

Neural network attracted more and more researchers for its abilities of parallel operation, self-learning, fault tolerance, associative memory, multifactorial optimization and extensibility [15-17]. Neural network based clustering has yielded good results [18, 19], yet the possibility of transforming the input space in order to facilitate segmentation has been largely unexplored [20].

Many approaches to MRI segmentation using neural network both supervised and unsupervised have been proposed in the literature [8, 9, 21-23]. Almost all types of neural networks have been applied with a different degree of success. The mostly used being Kohonen algorithm since it shows good segmentation accuracy in many segmentation based applications. In this method, classical Kohonen map-based clustering is enhanced through the search of an optimized space in which to operate the clustering [24, 25]. It allows for the ability to make the clustering methods able to retain more information from the original image than the crisp or hard segmentation methods [26].

The proposed model is based on the work as illustrated in [11] the network architecture consists of two fully interconnected layers; Each input voxel is formed as a feature vector as described by the pre-processing technique proposed in [10, 11, 27], the first layer, composed of computing elements of order zero with linear activation function, followed by a second layer of computing elements of order two, with gaussian activation function. Let X be the input pattern, H the output of the hidden layer and Y the output of the network. W and Z are the weight vectors of the first and second layer, respectively. In order to jointly optimize both layers, training is carried out in two steps. In the first step, the second layer is trained using the standard Kohonen rule for unsupervised learning at each iteration, the winning neuron's centers are adjusted according to equation 1.

$$\Delta Z_{ji} = \eta_z \cdot (H_i - Z_{ji}) \quad (1)$$

Where

ΔZ_{ji} = Change in weight vector

η_z = learning rate of the Kohonen layer

H_i = Out put of the ith neuron of the hidden layer

Z_{ji} = The weight vector of the Winning neuron

The weights of the neighboring neurons are updated according to equation 2.

$$\Delta Z_{ji} = \eta_z \cdot f_{neigh}(H_i - Z_{ji}) \quad (2)$$

Where

f_{neigh} = Gaussian activation function

Contrarily to the second layer, the first layer is trained using

Enhanced version of error back-propagation with the linear activation function, search of feature space. In supervised learning schemes, the error is given by equation 3.

$$E = \sum_p \|Y^p - T^p\|^2 \quad (3)$$

Where T^p is the user-supplied target associated to the P^{th} training pattern. Here the target is determined by associating each input pattern with the winning neuron. Intuitively, this corresponds to searching a linear transformation of the feature space, requiring that input patterns be as close as possible to the associated centroids. The hidden layer is then trained using the classical delta rule for training and is derived from equation 4.

$$\frac{\partial E}{\partial W_{ji}} = \sum_p \eta_p \sum_j (\delta_j^p \cdot x_i^p) \quad (4)$$

Where p denotes the p^{th} input pattern and

$$\delta_j^p = y_j^p - t_j^p$$

The weights of the first layer are then updated according to equation 5

$$\Delta W_{ij}(t+1) = -\eta_w \cdot \frac{\partial E}{\partial W_{ij}} + \mu \Delta W_{ij}(t) \quad (5)$$

$$\Delta W_{ij}(t) = \eta_w \delta_p H_j$$

Where

μ = momentum factor

η_w = learning rate of the Back propagation layer

The momentum term introduces the old weight change as a parameter for the computation of the new weight change. Momentum allows the net to make reasonably large weight adjustments as long as the corrections are in the same general direction for several patterns. Using smaller learning rate prevents a large response to the error from any training pattern.

The input layer is fed with a 5 dimensional feature vector followed by the first layer consists of 4 computing elements with linear activation function. Thus, not only the hidden layer performs a linear transformation of the input space, but it also reduces the dimensionality of the feature space. This allows obtaining, in average, better experimental results than when all features are retained in the clustering step. The second layer has 5 computing elements. Five clusters are sufficient to discriminate between adipose tissue, glandular tissue, ducts, air, benign or malignant masses. The network is separately trained for each image to account for inhomogeneities in intensity across different images by randomly selecting pixels per image as the training set. A Gaussian neighborhood function f_{neigh} equal to $0.01A^2e$ is used for unsupervised training. An adaptive learning coefficient is initially set to 0.0001 for the first layer as η_w and 0.001 for the second one as η_z . If the error increases, η is decreased and weight values are set to those of the previous iteration, whereas if the error decreases below a predefined threshold,

η is increased. Finally, training is stopped when a predetermined level of error is reached. The enhanced SOM based k-means clustered output image is then edge enhanced by unsharp filter as illustrated in [28] which is used to extract the edges of the tumour and by using proper thresholding as discussed in [29] the tumour or mass is extracted from the edge enhanced image.

B. Artificial Bee Colony Algorithm based Clustering

The Bees algorithm performs a kind of neighbourhood search combined with random search in a way that is indicative of the food foraging behavior of swarms of honey bees. In the artificial bee colony (ABC) algorithm, the colony of artificial bees contains three groups of bees: employed bees, onlookers and scouts. Each cycle of the search consists of three major steps: (1) placing the employed bees onto the food sources and then calculating their nectar amounts; (2) selecting the food sources by the onlookers after sharing the information of employed bees and determining the nectar amount of the food sources; (3) determining the scout bees and placing them onto the randomly determined food sources. In the ABC, a food source position represents a possible solution to the problem to be optimized and the nectar amount of a food source corresponds to the quality (fitness) of the associated solution [30, 31].

Swarm Intelligence is an innovative distributed intelligent model for solving optimization problems that originally took its inspiration from the biological examples by swarming. The artificial swarm bee colony clustering method exploits the search capability of the Bees Algorithm. Explicitly, the task is to search for appropriate cluster centres (c_1, c_2, \dots, c_k) such that the clustering metric Euclidean distance (equation 6) is minimised.

$$E = \sum_{j=1}^k \sum_{i=1}^n \left\| x_i^{(j)} - c_j \right\|^2 \quad (6)$$

Where $x_i^{(j)}$ is the i^{th} data point belonging to the j^{th} cluster, c_j is the centre of the j^{th} cluster, k is the number of clusters and n is the number of data points in cluster j . The basic steps of this clustering operation are:

Pseudo code of the ABC Algorithm

1: Initialize the population of solutions

2: Evaluate the fitness of the population.

In order to calculate the fitness values of solutions we employed the following equation 7.

$$fit_i = \begin{cases} \frac{1}{1 + f_i} & \text{if } f \geq 0 \\ 1 + abs(f_i) & \text{if } f < 0 \end{cases}$$

3: cycle=1

4: repeat while (stopping criteria not met) (7)

5: Produce new solutions

6: Select sites for neighbourhood search by means of information in the neighbourhood of the present one.

7: Recruit bees for selected sites (more bees for the best e sites) and evaluate fitness values.

Calculate the probability values P_i for the solutions by means

of their fitness values using the equation 8.

$$P_i = \frac{fit_i}{\sum_{i=1}^{SN} fit_i} \quad (8)$$

8: Select the fittest bee from each site.

9: Assign remaining bees to search randomly and evaluate their fitness values.

10: cycle=cycle+1

End While (Maximum number of cycles is reached)

The proposed segmentation method is based on the work as illustrated in [12]; the important part of any image processing system is represented by the preprocessing phase. The application of median filter over the image aims at compensating the effects of random noise, while minimizing the loss of resolution. The artificial bee colony clustering is used for clustering the pre-processed image. In the proposed ABC algorithm for clustering, each bee represents a potential clustering solution as set of k cluster centers, for clustering the breast DCE-MR image five clusters are sufficient to discriminate between adipose tissue, glandular tissue, ducts, air, benign or malignant masses, and the value of k can be assigned to five. Each site represents the patterns or data objects. The algorithm requires some parameters to be set, namely: number of scout bees (n), number of sites selected for neighbourhood searching (m), number of top-rated (elite) sites among m selected sites (e), number of bees recruited for the best e sites (nep), number of bees recruited for the other (me) selected sites (nsp), and the stopping criterion for the loop. The parameter values used in the proposed artificial bee colony clustering based segmentation algorithm implementation. The values were decided empirically

At the initialization stage, a set of scout bee population (n) are randomly selected to define the k clusters. The Euclidean distances between each data pattern and all centres are calculated to determine the cluster to which the data pattern belongs. In this way, initial clusters can be constructed. After the clusters have been formed, the original cluster centres are replaced by the actual centroids of the clusters to define a particular clustering solution. This initialization process is applied each time new bees are to be created.

In step 2, the fitness computation process is carried out for each site visited by a bee by equation 7. Step 5, is the main step of bee colony optimization, which start by forming the new population. In step 6, the m sites with the highest fitness are designated as selected sites and chosen for neighbourhood search. In steps 7 and 8, the algorithm performs searches around the selected sites, assigning more bees to search in the neighbourhood of the best e sites. Selection of the best sites can be made directly according to the fitness associated with them. Otherwise, the fitness values are used to determine the probability of the sites being selected using the equation 8. Searches in the neighbourhood of the best e sites - those which represent the most promising solutions, this is done by recruiting more bees for the best e sites than for the other selected sites. Together with scouting,

this differential recruitment is a key operation of the bee algorithm. In step 8, only the bee that has found the site with the highest fitness will be selected to form part of the next bee population. In nature, there is no such a restriction. This restriction is introduced here to reduce the number of points to be explored. In step 9, the remaining bees in the population are assigned randomly around the search space to scout for new potential solutions. At the end of each loop, the colony will have two stages to its new population: representatives from the selected sites, and scout bees assigned to conduct random searches. These steps are repeated until a stopping criterion is met. The standard deviation and the mean of the fitness value are calculated to study the performance of this algorithm. The honeybee clustered output image is then edge enhanced by unsharp filter as illustrated in [28], which is used to extract the edges of the tumor and by using proper thresholding as discussed in [29], the tumour or mass is extracted from the edge enhanced image.

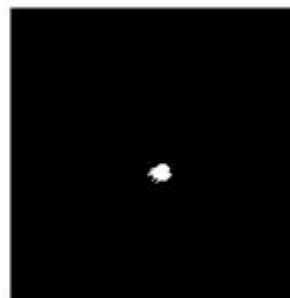
III. EXPERIMENTAL RESULTS AND DISCUSSION

In this section, the results obtained using real DCE- MR images are illustrated in figure 1. The breast DCE-MR images used in this study were acquired with patients prone to 1.5Tesla Siemens MRI scanner with the use of a dedicated surface breast coil array. The imaging protocol included bilateral fat suppressed T1 weighted images in the sagittal plane of 1mm slice thickness and a slab interleaved 3D fat suppressed spoiled gradient echo after the injection of contrast. One slice can contain 512×512 pixels. Ultimately, the effectiveness of the segmentation technique is to determine the extent to which potential abnormalities can be extracted from corresponding breast MRI based on its analysis. Real breast DCE-MR image used in this study were received from KMCH (Kovai Medical Center and Hospital), Coimbatore.

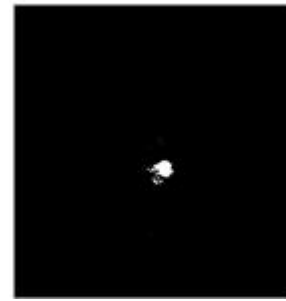
The breast DCE- MR image is first clustered using one of the clustering techniques discussed above in this paper. The clustered image corresponds to five regions which are adipose tissue, glandular tissue, ducts, air, benign or malignant masses, followed by edge enhancement and proper thresholding the mass or lesion is segmented separately. Then the segmented image will be compared to the reference image which is manually segmented by radiologist to measure the segmentation accuracy.



(a) Input image

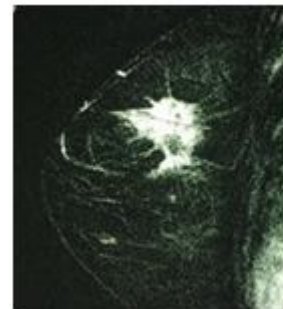


(b) Artificial bee-colony segmentation algorithm output

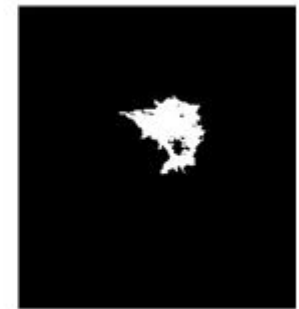


(c) Enhanced SOM based K-means segmentation algorithm output

Fig. 1. A representative original breast DCE-MR image with tumor obtained from 1.5Telsa MRI and the corresponding results of segmentation algorithms.



(a) Input image



(b) Artificial bee-colony segmentation algorithm output



(c) Enhanced SOM based K-means segmentation algorithm output

Fig. 2. A representative simulated breast DCE-MRI image with tumor obtained from the Internet in order to show that how the segmentation algorithms are adaptable irrelevant of the type of image, the corresponding results of segmentation algorithms.

It is clear from Fig. 1(a-c) and Fig.2 (a-c) that the artificial bee colony clustering algorithm based segmentation method completely succeeded in classifying the breast data. The other enhanced SOM based K-means clustering based segmentation algorithm partially corrected the misclassified pixels. As can be seen, the clustering results of artificial bee colony clustering algorithm were superior to enhanced SOM based K-means clustering algorithm.

A. Performance Measure

An objective method is needed to evaluate the performance of image segmentation algorithms so that the two algorithms can be compared. The most important performance criteria are accuracy, That is, the degree to which an algorithm's segmentation matches some reference manual segmentation.

The abnormal image pairs were used for testing the proposed algorithm to measure performance. The true positive detection rate and the number of false positive detection rate at various thresholds of the images are used to measure the algorithm's performance. These rates are represented using Receiver Operating Characteristic (ROC) curves. True Positive (TP) and False Positive (FP) rates are calculated at different thresholds selected on image pixels to generate an ROC curve and the best solution has been plotted for both the algorithm as illustrated in figure.3

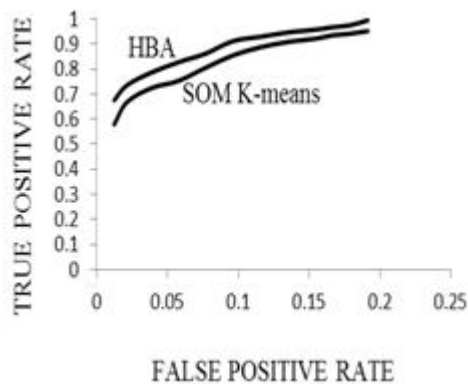


Figure 3. Illustrates the ROC curve of artificial bee colony clustering and enhanced k-means clustering algorithms.

TABLE I. PARAMETERS ACQUIRED FROM SEGMENTATION ALGORITHMS

Image	Algorithm Type	Standard Deviation	Tumor size in pixels	Accuracy
Image1	Enhanced SOM based K-means Algorithm	0.335	315	96.521
	Artificial Bee Colony Algorithm	0	290	99.667
Image2	Enhanced SOM based K-means Algorithm	0.437	2983	91.083
	Artificial Bee Colony Algorithm	0	3204	97.898

The bee colony clustering algorithm is a robust algorithm as indicated by the standard deviations of this algorithm is zero, but enhanced SOM based k-means clustering is not robust and this clustering approach also fails to achieve a high degree of accuracy for segmentation. It is well-known that the training speed depends on the choice of the learning rate. Trapping a local minimum and slow convergence rate are drawbacks of SOM based K-means algorithm. The sensitivity of the artificial bee colony algorithm is high since its accuracy is high as indicated in table 1. The adaptability of the algorithm can be assured by testing the algorithm over both real and simulated breast DCE-MR images, which results in different categories of image acquisition as illustrated in figure 2 where the simulated image from internet is used to prove that how these algorithms are adaptable to variability

of images. As exemplified in the figure. 2 and table 1, it is clear that the artificial bee colony algorithm is more adaptable to variability of images since its accuracy is 97.898% and the shape of the abnormal tissue around the lesion area is shown in detail, whereas for enhanced SOM based k-means algorithm achieved an accuracy of 91.083%.

The ABC algorithm is able to provide the same partition of image in all runs which makes it more reliable but the enhanced SOM based K-means algorithm is not reliable because it does not provide same partition of image in all runs. The efficiency of the ABC algorithm is good, since the time required is only 120 seconds and space required is also less but the execution time require in enhanced SOM based k-means depends on the convergence of error criteria. Evaluating the results obtained by both the algorithms, it's found that the best results obtained when using artificial bee colony clustering algorithm. ABC-based breast DCE-MRI segmentation algorithms are recognized useful in reducing image noise effects. According to the comparisons, the ABC provided refined accurate segmentation image with detail abnormal tissue. The iteration number to convergence is faster than the other algorithm. This shows that the ABC algorithm is a better choice as an aid to breast cancer medical diagnosis. The proposed two algorithms were implemented using matlab 7.5.

CONCLUSIONS

This paper has presented a comparison of two tissue segmentation algorithms that are currently widely used by researchers for segmentation of breast DCE-MR Images. Magnetic resonance imaging is increasingly employed for the depiction of human soft tissues, most notably the women breast. Computer-assisted image analysis techniques lead to image enhancement and automatic detection of anatomical structure. There are many methods that exist to segment the breast. Automatic segmentation of MRI volumes of the breast DCE-MRI is a complex task. The clinical acceptance of these methods will greatly depend on the accuracy of the segmentation, ease of computation and the reduction of operator dependence on their performance. From the implementation of two intelligent segmentation techniques in the subject of breast DCE- MR images, and analysing the results and quantitative comparison between these techniques. While both algorithms performed quite satisfactorily, the segmentation algorithm based on artificial bee colony was found on average to be more accurate, consistent, speedy convergence and robust than the algorithm implemented using enhanced SOM based k-means for breast DCE-MRI segmentation in our experiments.

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